

Sequence Listing

<110> ASHKENAZI, AVI J
 BOTSTEIN, DAVID
 DODGE, KELLY H.
 GURNEY, AUSTIN L.
 KIM, KYUNG JIN
 LAWRENCE, DAVID A.
 PITTI, ROBERT
 ROY, MARGARET A
 TUMAS, DANIEL B
 WOOD, WILLIAM I.

<120> Dcr3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289

<141> 1998-09-18

<150> US 60/059,288

<151> 1997-09-18

<150> US 60/094,640

<151> 1998-07-30

<160> 18

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<212> PRT

<213> Homo sapiens

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			20					25					30	

Ala	Glu	Thr	Pro	Thr	Tyr	Pro	Trp	Arg	Asp	Ala	Glu	Thr	Gly	Glu
			35					40					45	

Arg	Leu	Val	Cys	Ala	Gln	Cys	Pro	Pro	Gly	Thr	Phe	Val	Gln	Arg
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Pro	Cys	Arg	Arg	Asp	Ser	Pro	Thr	Thr	Cys	Gly	Pro	Cys	Pro	Pro
			65					70					75	

Arg	His	Tyr	Thr	Gln	Phe	Trp	Asn	Tyr	Leu	Glu	Arg	Cys	Arg	Tyr
			80					85					90	

Cys	Asn	Val	Leu	Cys	Gly	Glu	Arg	Glu	Glu	Glu	Ala	Arg	Ala	Cys	95	100	105
His	Ala	Thr	His	Asn	Arg	Ala	Cys	Arg	Cys	Arg	Thr	Gly	Phe	Phe	110	115	120
Ala	His	Ala	Gly	Phe	Cys	Leu	Glu	His	Ala	Ser	Cys	Pro	Pro	Gly	125	130	135
Ala	Gly	Val	Ile	Ala	Pro	Gly	Thr	Pro	Ser	Gln	Asn	Thr	Gln	Cys	140	145	150
Gln	Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Ala	Ser	Ser	Ser	Ser	Ser	155	160	165
Glu	Gln	Cys	Gln	Pro	His	Arg	Asn	Cys	Thr	Ala	Leu	Gly	Leu	Ala	170	175	180
Leu	Asn	Val	Pro	Gly	Ser	Ser	Ser	His	Asp	Thr	Leu	Cys	Thr	Ser	185	190	195
Cys	Thr	Gly	Phe	Pro	Leu	Ser	Thr	Arg	Val	Pro	Gly	Ala	Glu	Glu	200	205	210
Cys	Glu	Arg	Ala	Val	Ile	Asp	Phe	Val	Ala	Phe	Gln	Asp	Ile	Ser	215	220	225
Ile	Lys	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu	Ala	Pro	Glu	230	235	240
Gly	Trp	Gly	Pro	Thr	Pro	Arg	Ala	Gly	Arg	Ala	Ala	Leu	Gln	Leu	245	250	255
Lys	Leu	Arg	Arg	Arg	Leu	Thr	Glu	Leu	Leu	Gly	Ala	Gln	Asp	Gly	260	265	270
Ala	Leu	Leu	Val	Arg	Leu	Leu	Gln	Ala	Leu	Arg	Val	Ala	Arg	Met	275	280	285
Pro	Gly	Leu	Glu	Arg	Ser	Val	Arg	Glu	Arg	Phe	Leu	Pro	Val	His	290	295	300

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 <222> 1090

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atgagggcgc tggagggggc aggccgtgctg ctgctgtgcc tgggtgttggc 150
gctgcctgcc ctgctgccgg tgccggctgt acgcggagtg gcagaaacac 200
ccacctaccc ctggcgggac gcagagacag gggagcggct ggtgtgcgcc 250
cagtgcctcc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300
cacgacgtgt ggcccgtgtc caccgcgcca ctacacgcag ttctggaact 350
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gaggcacggg cttgccacgc caccacaaac cgtgcctgcc gctgccgcac 450
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cagccgtgcc ccccaggcac cttctcagcc agcagctcca gctcagagca 600
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ctttgtggct ttccaggaca tctccatcaa gaggctgcag cggctgctgc 800
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ggagcgtgag gaggaggcac gggcttgcca cgccaccac aaccgtgcct 150

gccgctgccg caccggttc ttcgcgcacg ctggtttctg cttggagcac 200

gcatcgtgtc cacctggtgc cggcgtgatt gcccgggca ccccagcca 250

gaacacgcag tgcctagccg tgccccccag gcaccttctc agccagcagc 300

tccagctcag agcagtgcc accccaccgc aactgcacgg ccttgggcct 350

ggccctcaat gtgccaggt cttcctcca tgacaccctg tgcaccagct 400

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cattctggaa ctacctggag cgc 73

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<213> Unknown

<220>

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<221> unsure

<223> unknown base

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ggagcgtgag gaggaggcan gngcttgcca cgccacccac aaccgcgcct 150

gcngctgcag caccggnttc ttgcgcacg ctgntttctg cttggagcac 200

gcacgtgtc cacctggtgn cggcgtgatt gncccgggca cccccagcca 250

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<211> 201

<212> DNA

<213> Unknown

<223> Unknown organism

<221> unsure

<222> 182

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gggagcgtga ggaggaggca cgggcttgcc acgccacca caaccgtgcc 100

tqccgctgcc gcaccggctt cttcgcgcac gctggtttct gcttggagca 150

cgcacgtgtt ccacctgggtg ccggcgtgat tnccccgggc acccccagcc 200

a 201

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<212> DNA

<213> Unknown

<223> Unknown organism

<220>
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gggccagcc ttgcacctg agctaggaca ccagttcccc tgacctgtt 100
cttccctcct ggtgcaggc acccccagcc agaacacgca gncagccgt 150
gccccccagg caccttctca gccagcagct ccagctcaga gcagtgccag 200
ccccaccgca actgcacggc cctgggcctg gccctcaatg tgccaggctc 250
ttctcccat gacacctgt gcaccag 277

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<212> DNA
<213> Unknown

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gccctcaatg tgccaggctc ttctcccat gacacctgt gcaccagct 199

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 aggctcttcc tcccatgaca cgctgtgcac cagctgcact ggcttcccc 150
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 atgtgccagg ctcttctctcc catgacaccc tgtgcaccag ctgcactggc 200
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ccc 53

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<211> 17

<212> DNA

<213> Unknown

<220>

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<211> 16

<212> DNA

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Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr
                      35                      40                      45

Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly
                      50                      55                      60

Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
                      65                      70                      75

Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val
                      80                      85                      90

Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val
                      95                      100                      105

Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
                      110                      115                      120

Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg
                      125                      130                      135

Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
                      140                      145                      150

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala
                      155                      160                      165

Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg
                      170                      175                      180

Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
                      185                      190                      195

Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala
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09896096-06301

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His Thr Gln Pro	Thr Pro Glu Pro Ser	Thr Ala Pro Ser Thr Ser
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Phe Leu Leu Pro	Met Gly Pro Ser Pro	Pro Ala Glu Gly Ser Thr
245	250	255
Gly Asp Phe Ala	Leu Pro Val Gly Leu	Ile Val Gly Val Thr Ala
260	265	270
Leu Gly Leu Leu	Ile Ile Gly Val Val	Asn Cys Val Ile Met Thr
275	280	285
Gln Val Lys Lys	Lys Pro Leu Cys Leu	Gln Arg Glu Ala Lys Val
290	295	300
Pro His Leu Pro	Ala Asp Lys Ala Arg	Gly Thr Gln Gly Pro Glu
305	310	315
Gln Gln His Leu	Leu Ile Thr Ala Pro	Ser Ser Ser Ser Ser Ser
320	325	330
Leu Glu Ser Ser	Ala Ser Ala Leu Asp	Arg Arg Ala Pro Thr Arg
335	340	345
Asn Gln Pro Gln	Ala Pro Gly Val Glu	Ala Ser Gly Ala Gly Glu
350	355	360
Ala Arg Ala Ser	Thr Gly Ser Ser Asp	Ser Ser Pro Gly Gly His
365	370	375
Gly Thr Gln Val	Asn Val Thr Cys Ile	Val Asn Val Cys Ser Ser
380	385	390
Ser Asp His Ser	Ser Gln Cys Ser Ser	Gln Ala Ser Ser Thr Met
395	400	405
Gly Asp Thr Asp	Ser Ser Pro Ser Glu	Ser Pro Lys Asp Glu Gln
410	415	420
Val Pro Phe Ser	Lys Glu Glu Cys Ala	Phe Arg Ser Gln Leu Glu
425	430	435
Thr Pro Glu Thr	Leu Leu Gly Ser Thr	Glu Glu Lys Pro Leu Pro
440	445	450
Leu Gly Val Pro	Asp Ala Gly Met Lys	Pro Ser
455	460	

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 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 18

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				20					25					30	
Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	
				35					40					45	
Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	
				50					55					60	
Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	
				65					70					75	
Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	
				80					85					90	
Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	
				95					100					105	
Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	
				110					115					120	
His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	
				125					130					135	
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	
				140					145					150	
Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	
				155					160					165	
Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	
				170					175					180	
His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	
				185					190					195	
Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	
				200					205					210	
Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	
				215					220					225	

05996096-063801

Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
 245 250 255

Leu Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile
 260 265 270

Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
 275 280 285

Gly His Ala Asn Leu Thr Phe Glu
 290

09896096-062801